

SEQUENCE LISTING

<110> Sagami Chemical Research Center,

Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these
proteins

<130> 661924

<150> JP 11-178065

<151> 1999-06-24

<160> 24

<210> 1

<211> 238

<212> PRT

<213> Homo sapiens

<400> 1

Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val Asp Met

1

5

10

15

Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe Thr Gly

20

25

30

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Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu Lys Thr
35 40 45

Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu Gln Val
50 55 60

Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn Ala Leu
65 70 75 80

Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn Lys Gly
85 90 95

Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met Asp Ile
100 105 110

Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr Leu Phe
115 120 125

Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His Thr His
130 135 140

Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn Thr Glu
145 150 155 160

Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu Ile Val
165 170 175

Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu Leu Ile
180 185 190

Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His Cys Ala
195 200 205

Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys Met Gly
210 215 220

Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser

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225

230

235

<210> 2

<211> 339

<212> PRT

<213> Homo sapiens

<400> 2

Met Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu

1

5

10

15

Gly Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn

20

25

30

Asp Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His

35

40

45

Tyr Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu

50

55

60

Lys Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val

65

70

75

80

Ile Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu

85

90

95

Cys Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val

100

105

110

Ser Cys Glu Gly Tyr Glu Ser Ser Glu Asp Gln Tyr Val Leu Arg Gly

115

120

125

Ser Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln

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130 135 140
Lys Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp
145 150 155 160
Tyr Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu
165 170 175
Ile Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu
180 185 190
Phe Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro
195 200 205
Pro Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro
210 215 220
Pro Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His
225 230 235 240
Gly Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr
245 250 255
Glu Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile
260 265 270
Leu Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp
275 280 285
Ser Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn
290 295 300
Arg Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys
305 310 315 320
Ser Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr
325 330 335

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Arg Arg Arg

<210> 3

<211> 326

<212> PRT

<213> Homo sapiens

<400> 3

Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln Arg Thr Leu

1 5 10 15

Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser Thr Thr Ser

20 25 30

Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val Pro Lys Pro

35 40 45

Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met Pro Val Ser

50 55 60

Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val Gln Tyr Asn

65 70 75 80

Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe Arg Ser Gly

85 90 95

Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly Glu Arg Cys

100 105 110

Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu Ile Leu Trp

115 120 125

Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln Phe Ile Ser

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130 135 140
Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn Pro Ala Cys
145 150 155 160
Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val Leu Ser Gly
165 170 175
Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val Phe Gln Ala
180 185 190
Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val Trp Asn Tyr
195 200 205
Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys Cys Met Ala
210 215 220
Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val Leu Glu Phe
225 230 235 240
Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn Cys Leu Pro
245 250 255
His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala Ala Pro Thr
260 265 270
Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln Pro Ile His
275 280 285
Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg Asn Lys Gly
290 295 300
Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val Arg Ser Ser
305 310 315 320
Val Glu Glu Glu Gln Cys

325

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<210> 4

<211> 324

<212> PRT

<213> Homo sapiens

<400> 4

Met Ala Ala Ala Ala Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu

1 5 10 15

Leu Leu Leu Phe Leu Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg

20 25 30

Ala Gly Pro Asp Glu Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala

35 40 45

Pro Ala Gln Gln Leu Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu

50 55 60

Pro Ala Arg Val Glu Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr

65 70 75 80

Asn Lys Glu Asp Pro Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala

85 90 95

Phe Val Ala Ala Ile Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys

100 105 110

Thr Phe Phe Ile Ala Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr

115 120 125

Val Leu Ala Gly Ala Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser

130 135 140

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Val Leu Phe Gly Tyr Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr
145 150 155 160
Tyr Val Ser Thr Val Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg
165 170 175
Glu Gly Leu Lys Met Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu
180 185 190
Val Gln Ala Glu Leu Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys
195 200 205
Leu Leu Asn Gly Pro Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val
210 215 220
Pro Gln Lys Lys Trp Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala
225 230 235 240
Leu Thr Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr
245 250 255
Thr Ile Val Leu Ala Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly
260 265 270
Gly Thr Val Gly His Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly
275 280 285
Arg Met Ile Ala Gln Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly
290 295 300
Gly Ile Val Phe Leu Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro
305 310 315 320
Asp Ser Gly Phe

<210> 5

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<211> 153

<212> PRT

<213> Homo sapiens

<400> 5

Met Asn Val Gly Thr Ala His Ser Glu Val Asn Pro Asn Thr Arg Val

1 5 10 15

Met Asn Ser Arg Gly Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu

20 25 30

Leu His Ile Val Leu Leu Ser Ile Pro Phe Val Ser Val Pro Val Val

35 40 45

Trp Thr Leu Thr Asn Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu

50 55 60

His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala

65 70 75 80

Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr

85 90 95

Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu

100 105 110

Thr Ser Phe Tyr Thr Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr

115 120 125

Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly

130 135 140

Val Arg Ile Phe Gly Ile Asn Lys Tyr

145 150

10/41

<210> 6

<211> 153

<212> PRT

<213> Homo sapiens

<400> 6

Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val

1 5 10 15

Met Asn Ser Arg Gly Ile Trp Leu Ala Tyr Ile Ile Leu Val Gly Leu

20 25 30

Leu His Met Val Leu Leu Ser Ile Pro Phe Phe Ser Ile Pro Val Val

35 40 45

Trp Thr Leu Thr Asn Val Ile His Asn Leu Ala Thr Tyr Val Phe Leu

50 55 60

His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala

65 70 75 80

Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu Gln Phe Thr

85 90 95

Ser Ser Arg Lys Phe Leu Ser Ile Ser Pro Ile Val Leu Tyr Leu Leu

100 105 110

Ala Ser Phe Tyr Thr Lys Tyr Asp Ala Ala His Phe Leu Ile Asn Thr

115 120 125

Ala Ser Leu Leu Ser Val Leu Leu Pro Lys Leu Pro Gln Phe His Gly

130 135 140

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Val Arg Val Phe Gly Ile Asn Lys Tyr

145

150

<210> 7

<211> 200

<212> PRT

<213> Homo sapiens

<400> 7

Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala

1

5

10

15

Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp

20

25

30

Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe

35

40

45

Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg

50

55

60

Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu

65

70

75

80

Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val

85

90

95

Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe

100

105

110

Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser

115

120

125

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Leu Ala Phe Thr Lys Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val

130

135

140

Pro Leu Pro Pro Lys Gly Arg Val Leu Ile His Trp Met Thr Leu Cys

145

150

155

160

Gln Thr Gln Met Lys Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met

165

170

175

Phe Gly Ile Leu Asn Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr

180

185

190

Leu Glu Lys Thr Ile His Glu Glu

195

200

<210> 8

<211> 189

<212> PRT

<213> Homo sapiens

<400> 8

Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Gly Ala Trp Ala

1

5

10

15

Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro

20

25

30

Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu

35

40

45

Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu

50

55

60

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Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg

65 70 75 80

Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser

85 90 95

Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg

100 105 110

Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val

115 120 125

Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu

130 135 140

His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln

145 150 155 160

Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly

165 170 175

Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu

180 185

<210> 9

<211> 714

<212> DNA

<213> Homo sapiens

<400> 9

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aacattgctc cccggattct caccaatttc actggagtaa tgccacctca gttcaaaaag 120

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gatttggatt cctatcttaa aactcgatca ccagtcactt tcctgtctga tctgcgcagc 180
 aacctacagg tatccaatga acctgggaat cgctacaacc tccagctcat caatgcactg 240
 gtgctctatg tcgggactca ggccattgcg cacatccaca acaagggcag cacaccttca 300
 atgagcacca tcactcactc agcacacatg gatatcttcc agaatttggc tgtggacttg 360
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 agccacactc actacttcag ttgcaccatg ctgtacctt ttgcagaggc caatacggaa 480
 gccatccaag aacagatcac aagagttctc ttggaacggt tgattgtaa taggccacat 540
 ccttggggtc ttcttattac cticattgag ctgattaaaa acccagcgtt taagttcttg 600
 aaccatgaat ttgtacactg tgccccagaa atcgaaaagt tattccagtc ggtcgcacag 660
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<210> 10

<211> 1017

<212> DNA

<213> Homo sapiens

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 gatgtaaaag ctcttaccct ccactatgac cgctatacca cctcccgcag gctggatccc 180
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 gaagaccagt atgtactaag aggttcttgt ggcttggagt ataattttaga ttatacagaa 420
 cttggcctgc agaaaactgaa ggagtctgga aagcagcacg gctttgcctc tttctctgat 480

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tattattata agtggctctc ggcggtattcc tgtaacatga gtggattgat taccatcgtg 540
gtactccttg ggatcgctt tgtagtctat aagctgttcc tgagtgcagg gcagtattct 600
cctccaccgt actctgagta tcctccattt tcccaccgtt accagagatt caccaactca 660
gcaggacctc ctccccagg ctttaagtct gagttcacag gaccacagaa tactggccat 720
ggtgcaactt ctggttttgg cagtgccttt acaggacaac aaggatatga aaattcagga 780
ccagggttct ggacaggctt gggaactggg ggaatactag gatatttgtt tggcagcaat 840
agagcggcaa cacccttctc agactcgtgg tactaccgt cctatcctcc ctctaccct 900
ggcacgtgga atagggctta ctacccctt catggaggct cgggcagcta ttcggtatgt 960
tcaaactcag acacgaaaac cagaactgca tcaggatatg gtggtaccag gagacga 1017

<210> 11

<211> 978

<212> DNA

<213> Homo sapiens

<400> 11

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ggcacacaga aggtgccccaa gccctgtgc gagaaaggtc tggcagccaa gtgctttgac 180
atgccagtgt ccctggatgg agataccaac acatccacc aggaggtggg acaatacaac 240
tgggagactg gggatgaccg gttctccttc cggagcttcc ggagtggcat gtggctatcc 300
tgtgaggaaa ctgtggaaga accaggggag aggtgccgaa gtttcattga acttacacca 360
ccagccaaga gagaaatcct atggttatcc ctgggaacgc agatcaccta catcggaatt 420
caattcatca gttcctcct gctactaaca gacttgctac tcaactgggaa ccctgcctgt 480
gggtcctaac tgagcgctt tgctgctgtt tcctctgtcc tgtcaggctt cctggggatg 540

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gtggcccaca tgatgtattc acaagtcttc caagcgactg tcaacttggg tccagaagac 600
tggagaccac atgtttggaa ttatggctgg gccttctaca tggcctggct ctccttcacc 660
tgctgcatgg cgtcggctgt caccaccttc aacacgtaca ccaggatggt gctggagttc 720
aagtgcagc atagtaagag cttcaaggaa aaccggaact gcctaccaca tcaccatcag 780
tgtttccctc ggcggtgtgc aagtgcagcc cccaccgtgg gtcccttgac cagctaccac 840
cagtatcata atcagcccat ccactctgtc tctgagggag tcgacttcta ctccgagctg 900
cggaacaagg gatttcaaag aggggccagc caggagctga aagaagcagt taggtcatct 960
gtagaggaag agcagtgt 978

<210> 12

<211> 972

<212> DNA

<213> Homo sapiens

<400> 12

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caccggaaca aagaaccgcc ggcgccggcc cagcagctgc agccgcagcc tgtggctgtg 180
cagggccccg agccggcccc ggtcgagaaa atatttacac cagcagctcc agttcatacc 240
aataaagaag atcctgctac ccaaactaat ttgggattta tccatgcatt tgctgctgcc 300
atatcagtta ttattgtatc tgaattgggt gataagacat tttttatagc agccatcatg 360
gcaatgcgct ataaccgctt gaccgtgctg gctgggtgaa tgcttgctt gggactaatg 420
acatgcttgt cagttttgtt tggctatgcc accacagtca tccccagggt ctatacatc 480
tatgtttcaa ctgtattatt tgccattttt ggcattagaa tgcttcggga aggcttaaag 540
atgagccctg atgagggtca agaggaactg gaagaagttc aagctgaatt aaagaagaaa 600

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gatgaagaat ttcaacgaac caaactttta aatggaccgg gagatgttga aacgggtaca      660
agcataacag tacctcagaa aaagtgggtg ctttttattt cacccatttt tgttcaagct      720
cttacattaa cattcttagc agaatggggt gatcgctctc aactaactac aattgtattg      780
gcagctagag aggacccta tgggtgtagcc gtgggtggaa ctgtggggca ctgcctgtgc      840
acgggattgg cagtaattgg aggaagaatg atagcacaga aaatctctgt cagaactgtg      900
acaatcatag gaggcacgtg ttttttggcg tttgcatttt ctgcactatt tataagccct      960
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<210> 13

<211> 459

<212> DNA

<213> Homo sapiens

<400> 13

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ccgtttgtga gtgtccctgt cgtctggacc ctcaccaacc tcattcacia catgggcatg      180
tatatcticc tgcacacggt gaaggggaca ccccttgaga ccccggaaca gggcaaggcg      240
aggctgctaa cccactggga gcagatggat tatgggggtc agttcacggc ctctcggaag      300
ttcttgacca tcacacccat cgtgctgtac ttcctcacca gcttctacac taagtacgac      360
cagatccatt ttgtgtcaa caccgtgtcc ctgatgagcg tgcttatccc caagctgccc      420
cagctccacg gagtccggat ttttggaatc aataagtac                                459

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<210> 14

<211> 459

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<212> DNA

<213> Homo sapiens

<400> 14

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cccttcttca gcattcctgt tgtctggacc ctgaccaacg tcatccataa cctggctacg      180
tatgtcttcc ttcatacggg gaaagggaca cccttgaga ctctgacca aggaaaggct      240
cggctactga cacactggga gcaaattggac tatgggctcc agtttacctc tccccgaag      300
ttcctcagca tctctcctat tgtgctctat ctctggcca gttctatac caagtatgat      360
gctgcgcact tctcatcaa cacagcctca ttgctaagtg tactgctgcc gaagttgccc      420
cagttccatg gggttcgtgt ctttggcatc aacaatac      459
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<210> 15

<211> 600

<212> DNA

<213> Homo sapiens

<400> 15

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atggcagcat ctatgcatgg tcagcccagt ctttctctag aagatgcaaa actcagaaga      60
ccaatggtca tagaaatcat agaaaaaaat ttgactatc ttagaaaaga aatgacacaa      120
aatatatatc aaatggcgac atttggaca acagctgggt tctctggaat attctcaaac      180
ttcctgttca gacgtgctt caaggttaaa catgatgctt tgaagacata tgcattcattg      240
gctacacttc catttttgc tactgttgtt actgacaagc tttttgtaat tgatgctttg      300
tattcagata atataagcaa ggaaaactgt gttttcagaa gctcactgat tggcatagtt      360
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tgtggtgttt tctatcccag ttctttggct ttactaaaa atggacgcct ggcaaccaag 420
tatcataccg ttccactgcc accaaaagga agggtttta tccattggat gacgctttgt 480
caaacacaaa tgaaattaat ggcgattcct ctagtctttc agattatgtt tggaatatta 540
aatggtctat accattatgc agtatttgaa gagacacttg agaaaactat acatgaagag 600

<210> 16

<211> 567

<212> DNA

<213> Homo sapiens

<400> 16

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ctcggggaca gggcgccact cacagccaca gccccacaac tggatgatga ggagatgtac 120
tcagcccaca tgcccgtca cctgcgctgt gatgcctgca gagctgtggc ttaccagatg 180
tggcaaaatc tggcaaaggc agagaccaa cttcatacct caaactctgg gggcgggcgg 240
gagctgagcg agttggtcta cacggatgtc ctggaccgga gctgctcccg gaactggcag 300
gactacggag ttcgagaagt ggaccaagt aaacgtctca caggcccagg acttagcgag 360
gggccagagc caagcatcag cgtgatggc acagggggcc cctggcctac caggctctcc 420
aggacatgtt tgcactactt gggggagttt ggagaagacc agatctatga agcccaccaa 480
caaggccgag gggctctgga ggcattgcta tgtggggggac cccagggggc ctgctcagag 540
aaggtgtcag ccacaagaga agagctc 567

<210> 17

<211> 1167

<212> DNA

20/41

<213> Homo sapiens

<220>

<221> CDS

<222> (187)... (903)

<400> 17

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 ttcttctaaa gaaagaaaga ctgattaata aaatgtggca gctgtgctct tcaaggcatt 120
 tatagtgtat atagtttttag aaaaacagtc ccaccactta agcatagatg taatttacta 180
 ataaaa atg att ctg ctt gtg att ctt gca ttt tat ctg tgg cag gtg 228

Met Ile Leu Leu Val Ile Leu Ala Phe Tyr Leu Trp Gln Val

1 5 10

gac atg ttg agt gaa att aac att gct ccc cgg att ctc acc aat ttc 276

Asp Met Leu Ser Glu Ile Asn Ile Ala Pro Arg Ile Leu Thr Asn Phe

15 20 25 30

act gga gta atg cca cct cag ttc aaa aag gat ttg gat tcc tat ctt 324

Thr Gly Val Met Pro Pro Gln Phe Lys Lys Asp Leu Asp Ser Tyr Leu

35 40 45

aaa act cga tca cca gtc act ttc ctg tct gat ctg cgc agc aac cta 372

Lys Thr Arg Ser Pro Val Thr Phe Leu Ser Asp Leu Arg Ser Asn Leu

50 55 60

cag gta tcc aat gaa cct ggg aat cgc tac aac ctc cag ctc atc aat 420

Gln Val Ser Asn Glu Pro Gly Asn Arg Tyr Asn Leu Gln Leu Ile Asn

65 70 75

21/41

gca ctg gtg ctc tat gtc ggg act cag gcc att gcg cac atc cac aac	468
Ala Leu Val Leu Tyr Val Gly Thr Gln Ala Ile Ala His Ile His Asn	
80 85 90	
aag ggc agc aca cct tca atg agc acc atc act cac tca gca cac atg	516
Lys Gly Ser Thr Pro Ser Met Ser Thr Ile Thr His Ser Ala His Met	
95 100 105 110	
gat atc ttc cag aat ttg gct gtg gac ttg gac act gag ggt cgc tat	564
Asp Ile Phe Gln Asn Leu Ala Val Asp Leu Asp Thr Glu Gly Arg Tyr	
115 120 125	
ctc ttt ttg aat gca att gca aat cag ctc cgg tac cca aat agc cac	612
Leu Phe Leu Asn Ala Ile Ala Asn Gln Leu Arg Tyr Pro Asn Ser His	
130 135 140	
act cac tac ttc agt tgc acc atg ctg tac ctt ttt gca gag gcc aat	660
Thr His Tyr Phe Ser Cys Thr Met Leu Tyr Leu Phe Ala Glu Ala Asn	
145 150 155	
acg gaa gcc atc caa gaa cag atc aca aga gtt ctc ttg gaa cgg ttg	708
Thr Glu Ala Ile Gln Glu Gln Ile Thr Arg Val Leu Leu Glu Arg Leu	
160 165 170	
att gta aat agg cca cat cct tgg ggt ctt ctt att acc ttc att gag	756
Ile Val Asn Arg Pro His Pro Trp Gly Leu Leu Ile Thr Phe Ile Glu	
175 180 185 190	
ctg att aaa aac cca gcg ttt aag ttc tgg aac cat gaa ttt gta cac	804
Leu Ile Lys Asn Pro Ala Phe Lys Phe Trp Asn His Glu Phe Val His	
195 200 205	
tgt gcc cca gaa atc gaa aag tta ttc cag tcg gtc gca cag tgc tgc	852

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Cys Ala Pro Glu Ile Glu Lys Leu Phe Gln Ser Val Ala Gln Cys Cys

210

215

220

atg gga cag aag cag gcc cag caa gta atg gaa ggg aca ggt gcc agt 900

Met Gly Gln Lys Gln Ala Gln Gln Val Met Glu Gly Thr Gly Ala Ser

225

230

235

tagacgaaac tgcatctctg ttgtacgtgt cagtctagag gtctcactgc accgagttca 960

taaactgact gaagaatcct ttcagctctt cctgactttc ccagcccttt ggtttgtggg 1020

tatctgcccc aactactgtt gggatcagcc tctgtctta tgtgggcacg ttccaaagtt 1080

taaatgcatt tttttgactc ttggccaaaa tttagaagat gctgtgaata tcattttgaa 1140

cttgtgtaaa tacatgaaag agaaaac 1167

<210> 18

<211> 1925

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (115)... (1134)

<400> 18

gttccttcgc cgccgccagg ggtagcgggtg tagctgcgca gcgtcgcgcg cgctaccgca 60

cccaggttcg gcccgtaggc gtctggcage ccggcgccat cttcatcgag cgcc atg 117

Met

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gcc gca gcc tgc ggg ccg gga gcg gcc ggg tac tgc ttg ctc ctc ggc	165
Ala Ala Ala Cys Gly Pro Gly Ala Ala Gly Tyr Cys Leu Leu Leu Gly	
5 10 15	
ttg cat ttg ttt ctg ctg acc gcg ggc cct gcc ctg ggc tgg aac gac	213
Leu His Leu Phe Leu Leu Thr Ala Gly Pro Ala Leu Gly Trp Asn Asp	
20 25 30	
cct gac aga atg ttg ctg cgg gat gta aaa gct ctt acc ctc cac tat	261
Pro Asp Arg Met Leu Leu Arg Asp Val Lys Ala Leu Thr Leu His Tyr	
35 40 45	
gac cgc tat acc acc tcc cgc agg ctg gat ccc atc cca cag ttg aaa	309
Asp Arg Tyr Thr Thr Ser Arg Arg Leu Asp Pro Ile Pro Gln Leu Lys	
50 55 60 65	
tgt gtt gga ggc aca gct ggt tgt gat tct tat acc cca aaa gtc ata	357
Cys Val Gly Gly Thr Ala Gly Cys Asp Ser Tyr Thr Pro Lys Val Ile	
70 75 80	
cag tgt cag aac aaa ggc tgg gat ggg tat gat gta cag tgg gaa tgt	405
Gln Cys Gln Asn Lys Gly Trp Asp Gly Tyr Asp Val Gln Trp Glu Cys	
85 90 95	
aag acg gac tta gat att gca tac aaa ttt gga aaa act gtg gtg agc	453
Lys Thr Asp Leu Asp Ile Ala Tyr Lys Phe Gly Lys Thr Val Val Ser	
100 105 110	
tgt gaa ggc tat gag tcc tct gaa gac cag tat gta cta aga ggt tct	501
Cys Glu Gly Tyr Glu Ser Ser-Glu Asp Gln Tyr Val Leu Arg Gly Ser	
115 120 125	
tgt ggc ttg gag tat aat tta gat tat aca gaa ctt ggc ctg cag aaa	549

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Cys Gly Leu Glu Tyr Asn Leu Asp Tyr Thr Glu Leu Gly Leu Gln Lys
 130 135 140 145
 ctg aag gag tct gga aag cag cac ggc ttt gcc tct ttc tct gat tat 597
 Leu Lys Glu Ser Gly Lys Gln His Gly Phe Ala Ser Phe Ser Asp Tyr
 150 155 160
 tat tat aag tgg tcc tcg gcg gat tcc tgt aac atg agt gga ttg att 645
 Tyr Tyr Lys Trp Ser Ser Ala Asp Ser Cys Asn Met Ser Gly Leu Ile
 165 170 175
 acc atc gtg gta ctc ctt ggg atc gcc ttt gta gtc tat aag ctg ttc 693
 Thr Ile Val Val Leu Leu Gly Ile Ala Phe Val Val Tyr Lys Leu Phe
 180 185 190
 ctg agt gac ggg cag tat tct cct cca ccg tac tct gag tat cct cca 741
 Leu Ser Asp Gly Gln Tyr Ser Pro Pro Pro Tyr Ser Glu Tyr Pro Pro
 195 200 205
 ttt tcc cac cgt tac cag aga ttc acc aac tca gca gga cct cct ccc 789
 Phe Ser His Arg Tyr Gln Arg Phe Thr Asn Ser Ala Gly Pro Pro Pro
 210 215 220 225
 cca ggc ttt aag tct gag ttc aca gga cca cag aat act ggc cat ggt 837
 Pro Gly Phe Lys Ser Glu Phe Thr Gly Pro Gln Asn Thr Gly His Gly
 230 235 240
 gca act tct ggt ttt ggc agt gct ttt aca gga caa caa gga tat gaa 885
 Ala Thr Ser Gly Phe Gly Ser Ala Phe Thr Gly Gln Gln Gly Tyr Glu
 245 250 255
 aat tca gga cca ggg ttc tgg aca ggc ttg gga act ggt gga ata cta 933
 Asn Ser Gly Pro Gly Phe Trp Thr Gly Leu Gly Thr Gly Gly Ile Leu

25/41

260	265	270	
gga tat ttg ttt ggc agc aat aga gcg gca aca ccc ttc tca gac tcg			981
Gly Tyr Leu Phe Gly Ser Asn Arg Ala Ala Thr Pro Phe Ser Asp Ser			
275	280	285	
tgg tac tac ccg tcc tat cct ccc tcc tac cct ggc acg tgg aat agg			1029
Trp Tyr Tyr Pro Ser Tyr Pro Pro Ser Tyr Pro Gly Thr Trp Asn Arg			
290	295	300	305
gct tac tca ccc ctt cat gga ggc tcg ggc agc tat tcg gta tgt tca			1077
Ala Tyr Ser Pro Leu His Gly Gly Ser Gly Ser Tyr Ser Val Cys Ser			
310	315	320	
aac tca gac acg aaa acc aga act gca tca gga tat ggt ggt acc agg			1125
Asn Ser Asp Thr Lys Thr Arg Thr Ala Ser Gly Tyr Gly Gly Thr Arg			
325	330	335	
aga cga taaagtagaa agttggagtc aaacactgga tgcagaaatt ttggatttt			1180
Arg Arg			
tcataccttt ctcttttagaa aaaaagtact acctgttaac aattgggaaa aggggatatt			1240
caaaagtctt gtggtgttat gtccagtgt gctttttgta ttctattatt tgaggctaaa			1300
agttgatgtg tgacaaaata cttatgtgtt gtatgtcagt gtaacatgca gatgtatatt			1360
gcagtttttg aaagtgatca ttactgtgga atgctaaaaa tacattaatt tctaaaacct			1420
gtgatgccct aagaagcatt aagaatgaag gtgttgtact aatagaaact aagtacagaa			1480
aatttcagtt ttaggtggtt gtagctgatg agttattacc tcatagagac tataatatcc			1540
tatttggtat tatattattt gatgtttgct gttcttcaaa catttaaadc aagctttgga			1600
ctaattatgc taatttgtga gttctgatca cttttgagct ctgaagcttt gaatcattca			1660
gtggtggaga tggccttctg gtaactgaat attaccttct gtaggaaaag gtggaaaata			1720

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agcatctaga aggttgttgt gaatgactct gtgctggcaa aaatgcttga aacctctata 1780
 ttcttttctg tcataagagg taaagggtcaa atttttcaac aaaagtcttt taataacaaa 1840
 agcatgcagt tctctgtgaa atctcaaata ttgttgtaat agtctgtttc aatcttaaaa 1900
 agaatcaata aaaacaaaca agggg 1925

<210> 19

<211> 1125

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (71)... (1051)

<400> 19

ttaaaccaaa gggacttgga gtgcagatgg catccttcgg ttcttcaga caagctgcaa 60

gacgctgacc atg gcc aag atg gag ctc tcg aag gcc ttc tct ggc cag 109

Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln

1

5

10

cgg aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc ttc tcc 157

Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser

15

20

25

aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag aag gtg 205

Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val

30

35

40

45

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ccc aag ccc ctg tgc gag aaa ggt ctg gca gcc aag tgc ttt gac atg	253
Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp Met	
50 55 60	
cca gtg tcc ctg gat gga gat acc aac aca tcc acc cag gag gtg gta	301
Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val Val	
65 70 75	
caa tac aac tgg gag act ggg gat gac cgg ttc tcc ttc cgg agc ttc	349
Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe Arg Ser Phe	
80 85 90	
cgg agt ggc atg tgg cta tcc tgt gag gaa act gtg gaa gaa cca ggg	397
Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val Glu Glu Pro Gly	
95 100 105	
gag agg tgc cga agt ttc att gaa ctt aca cca cca gcc aag aga gaa	445
Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro Pro Ala Lys Arg Glu	
110 115 120 125	
atc cta fgg tta tcc ctg gga acg cag atc acc tac atc gga ctt caa	493
Ile Leu Trp Leu Ser Leu Gly Thr Gln Ile Thr Tyr Ile Gly Leu Gln	
130 135 140	
ttc atc agc ttc ctc ctg cta cta aca gac ttg cta ctc act ggg aac	541
Phe Ile Ser Phe Leu Leu Leu Leu Thr Asp Leu Leu Leu Thr Gly Asn	
145 150 155	
cct gcc tgt ggg ctc aaa ctg agc gcc ttt gct gct gtt tcc tct gtc	589
Pro Ala Cys Gly Leu Lys Leu Ser Ala Phe Ala Ala Val Ser Ser Val	
160 165 170	
ctg tca ggt ctc ctg ggg atg gtg gcc cac atg atg tat tca caa gtc	637

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Leu Ser Gly Leu Leu Gly Met Val Ala His Met Met Tyr Ser Gln Val
 175 180 185
 ttc caa gcg act gtc aac ttg ggt cca gaa gac tgg aga cca cat gtt 685
 Phe Gln Ala Thr Val Asn Leu Gly Pro Glu Asp Trp Arg Pro His Val
 190 195 200 205
 tgg aat tat ggc tgg gcc ttc tac atg gcc tgg ctc tcc ttc acc tgc 733
 Trp Asn Tyr Gly Trp Ala Phe Tyr Met Ala Trp Leu Ser Phe Thr Cys
 210 215 220
 tgc atg gcg tcg gct gtc acc acc ttc aac acg tac acc agg atg gtg 781
 Cys Met Ala Ser Ala Val Thr Thr Phe Asn Thr Tyr Thr Arg Met Val
 225 230 235
 ctg gag ttc aag tgc aag cat agt aag agc ttc aag gaa aac ccg aac 829
 Leu Glu Phe Lys Cys Lys His Ser Lys Ser Phe Lys Glu Asn Pro Asn
 240 245 250
 tgc cta cca cat cac cat cag tgt ttc cct cgg cgg ctg tca agt gca 877
 Cys Leu Pro His His His Gln Cys Phe Pro Arg Arg Leu Ser Ser Ala
 255 260 265
 gcc ccc acc gtg ggt cct ttg acc agc tac cac cag tat cat aat cag 925
 Ala Pro Thr Val Gly Pro Leu Thr Ser Tyr His Gln Tyr His Asn Gln
 270 275 280 285
 ccc atc cac tct gtc tct gag gga gtc gac ttc tac tcc gag ctg cgg 973
 Pro Ile His Ser Val Ser Glu Gly Val Asp Phe Tyr Ser Glu Leu Arg
 290 295 300
 aac aag gga ttt caa aga ggg gcc agc cag gag ctg aaa gaa gca gtt 1021
 Asn Lys Gly Phe Gln Arg Gly Ala Ser Gln Glu Leu Lys Glu Ala Val

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305 310 315
 agg tca tct gta gag gaa gag cag tgt taggagttaa gcgggtttgg gg 1070
 Arg Ser Ser Val Glu Glu Glu Gln Cys

320 325
 agtaggcttg agccctacct tacacgtctg ctgattatca acatgtgctt aagcc 1125

<210> 20

<211> 1734

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (40)... (1014)

<400> 20

ctcttgcggc gcccgtagcg gcgcggcccg gcaggcggg atg gcg gcc gcg gct 54

Met Ala Ala Ala Ala

1 5

ccg ggg aac ggc cgc gca tcg gcg ccc cgg ctg ctt ctg ctc ttt ctg 102

Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu Leu Leu Leu Phe Leu

10 15 20

gtt ccg ctg ctg tgg gcc ccg gct gcg gtc cgg gcc ggc cca gat gaa 150

Val Pro Leu Leu Trp Ala Pro Ala Ala Val Arg Ala Gly Pro Asp Glu

25 30 35

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gac ctt agc cac cgg aac aaa gaa ccg ccg gcg ccg gcc cag cag ctg	198
Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala Gln Gln Leu	
40 45 50	
cag ccg cag cct gtg gct gtg cag ggc ccc gag ccg gcc cgg gtc gag	246
Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala Arg Val Glu	
55 60 65	
aaa ata ttt aca cca gca gct cca gtt cat acc aat aaa gaa gat cct	294
Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys Glu Asp Pro	
70 75 80 85	
gct acc caa act aat ttg gga ttt atc cat gca ttt gtc gct gcc ata	342
Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val Ala Ala Ile	
90 95 100	
tca gtt att att gta tct gaa ttg ggt gat aag aca ttt ttt ata gca	390
Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe Phe Ile Ala	
105 110 115	
gcc atc atg gca atg cgc tat aac cgc ctg acc gtg ctg gct ggt gca	438
Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala	
120 125 130	
atg ctt gcc ttg gga cta atg aca tgc ttg tca gtt ttg ttt ggc tat	486
Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu Phe Gly Tyr	
135 140 145	
gcc acc aca gtc atc ccc agg gtc tat aca tac tat gtt tca act gta	534
Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val Ser Thr Val	
150 155 160 165	
tta ttt gcc att ttt ggc att aga atg ctt cgg gaa ggc tta aag atg	582

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Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly Leu Lys Met
 170 175 180
 agc cct gat gag ggt caa gag gaa ctg gaa gaa gtt caa gct gaa tta 630
 Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln Ala Glu Leu
 185 190 195
 aag aag aaa gat gaa gaa ttt caa cga acc aaa ctt tta aat gga ccg 678
 Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu Asn Gly Pro
 200 205 210
 gga gat gtt gaa acg ggt aca agc ata aca gta cct cag aaa aag tgg 726
 Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln Lys Lys Trp
 215 220 225
 ttg cat ttt att tca ccc att ttt gtt caa gct ctt aca tta aca ttc 774
 Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr Leu Thr Phe
 230 235 240 245
 tta gca gaa tgg ggt gat cgc tct caa cta act aca att gta ttg gca 822
 Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile Val Leu Ala
 250 255 260
 gct aga gag gac ccc tat ggt gta gcc gtg ggt gga act gtg ggg cac 870
 Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr Val Gly His
 265 270 275
 tgc ctg tgc acg gga ttg gca gta att gga gga aga atg ata gca cag 918
 Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met Ile Ala Gln
 280 285 290
 aaa atc tct gtc aga act gtg aca atc ata gga ggc atc gtt ttt ttg 966
 Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile Val Phe Leu

32/41

295	300	305	
gcg ttt gca ttt tct gca cta ttt ata agc cct gat tct ggt ttt			1011
Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro Asp Ser Gly Phe			
310	315	320	
taacgctgt ttgttcatct atatttagtt taaaataggt agtattatct ttctgtacat			1070
agtgtacatt acaactaaaa gtgatggaaa aatactgtat ttgttagcac tgattttgtg			1130
agtttgaccc attattatgt ctgagatata atcattgatt ctatttgtaa caaggagttt			1190
taaaagaaac ctgacttcta agtgtgggtt tttcttctct ccaacataat tatgttaata			1250
tggctcctcat ttttcttttg gtgcagaacc gttgtgcagt ggggtctacc atgcaatttt			1310
ctttcagcac tgaccctttt ttaaggaata caaattttct ctttcatcac ttaggtgttt			1370
taagatgttt accttaaagt ttttcttggg gaaagaatga attaatttct atttcttaaa			1430
acatttcctt gagccagtaa acagtagttt aatcattggt cttttcaaaa ctaggtgttt			1490
aaaaaaagag acatatatga tattgctgtt atatcaataa catggcacia caagaactgt			1550
ctgccaggtc attcttcttc tttttttttt aattgggtag gacaccaat ataaaaacag			1610
tcaatatttg acaatgtgga attaccaa ataaaagagaa tactatgaat gtattcatat			1670
tttttctata ttgaataaac aatgtaacat agataacaat ataaataaaa gtggtatgac			1730
cagt			1734

<210> 21

<211> 2064

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

33/41

<222> (98)... (559)

<400> 21

aaaacagctg ctggagcagc agcggccccc gctcccggga accgttcccg ggccgttgat	60
cttcggcccc acacgaacag cagagagggg cagcagg atg aat gtg ggc aca	112
Met Asn Val Gly Thr	
1 5	
gcg cac agc gag gtg aac ccc aac acg cgg gtg atg aac agc cgt ggc	160
Ala His Ser Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly	
10 15 20	
atc tgg ctc tcc tac gtg ctg gcc atc ggt ctc ctc cac atc gtg ctg	208
Ile Trp Leu Ser Tyr Val Leu Ala Ile Gly Leu Leu His Ile Val Leu	
25 30 35	
ctg agc atc ccg ttt gtg agt gtc cct gtc gtc tgg acc ctc acc aac	256
Leu Ser Ile Pro Phe Val Ser Val Pro Val Val Trp Thr Leu Thr Asn	
40 45 50	
ctc att cac aac atg ggc atg tat atc ttc ctg cac acg gtg aag ggg	304
Leu Ile His Asn Met Gly Met Tyr Ile Phe Leu His Thr Val Lys Gly	
55 60 65	
aca ccc ttt gag acc ccg gac cag ggc aag gcg agg ctg cta acc cac	352
Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His	
70 75 80 85	
tgg gag cag atg gat tat ggg gtc cag ttc acg gcc tct cgg aag ttc	400
Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr Ala Ser Arg Lys Phe	
90 95 100	

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ttg acc atc aca ccc atc gtg ctg tac ttc ctc acc agc ttc tac act 448
 Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu Thr Ser Phe Tyr Thr
 105 110 115
 aag tac gac cag atc cat ttt gtg ctc aac acc gtg tcc ctg atg agc 496
 Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr Val Ser Leu Met Ser
 120 125 130
 gtg ctt atc ccc aag ctg ccc cag ctc cac gga gtc cgg att ttt gga 544
 Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly Val Arg Ile Phe Gly
 135 140 145
 atc aat aag tac tgagagtga gcccttccc ctgccaggg tggcagggga gggg 600
 Ile Asn Lys Tyr
 150
 tagggtaaaa ggcattgtgt gcaacactga agacagaaag aagaagcctc tggacactgc 660
 cagagatggg ggttgagcct ctggcctaata tccccccctc gcttccccca gtagccaact 720
 tggagtagct ttagtggtggg ttggggtagg ccccttgggc tctgaccttt tctgaatttt 780
 ttgatctttt ccttttgcct tttgaataga gactccatgg agtttggtcat ggaatgggct 840
 gggctcctgg gctgaacatg gaccacgcag ttgcgcacagg aggccagggg aaaaaccctt 900
 gctcacttgt ttgccctcag gcagccaaag cactttaacc cctgcatagg gagcagaggg 960
 cggtacggct tctggattgt ttcactgtga ttcctagggt ttttcgatgc cacgcagtgt 1020
 gtgcttttgt gtatggaagc aagtgtggga tgggtctttg cttttctggg tagggagctg 1080
 tctaatacaa gtcccaggct tttggcagct tctctgcaac ccaccgtggg tcttggttgg 1140
 gagtggggag ggtcagggtg gggaaagatg gggtagagt tagatggctt ggttccagag 1200
 gtgagggggc cagggctgct gccatcctgg cctgggtggag gttggggagc tgtaggagag 1260
 ctagtgagtc gagacttaga agaattggggc cacatagcag cagaggactg gtgtaaggga 1320
 gggaggggta gggacagaag ctagaccaa tctcctttgg gatgtgggca gggaggggaag 1380

35/41

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caggcttgga gggtaattt acccacagaa tgtgatagta ataggggagg gaggctgctg 1440
tgggtttaac tcctgggttg gctgttgggt agacaggtgg ggaaaaggcc cgtgagtcac 1500
tgtaagcaca ggtccaactt ggccctgact cctgcggggg tatggggaag ctgtgacaga 1560
aacgatgggt gctgtggtcc tctgcaggcc ctcacccctt aacttcctca tacagactgg 1620
cactgggcag ggcctctcat gtggcagcca catgtggcgt tgtgaggcca ccccatgtgg 1680
ggtctgtggt gagagtcctg taggatccct gctcaagcag cacagaggaa ggggcaagac 1740
gtggcctgta ggcactgttt cagcctgcag agaagaaagt gaggccggga gcctgagcct 1800
gggctggagc cttctcccct cccagtttg actaggggca gtgttaattt tgaaaagggtg 1860
tgggtccctg tgcctcttc caggggtcca agggaacagg agaggtcact gggcctgttt 1920
tctccctcct gacctgcat ctcccacccc gtgtatcata gggaactttc accttaaaat 1980
ctttctaagc aaagtgtgaa taggattttt actccctttg tacagtattc tgagaaacgc 2040
aaataaaagg gcaacatgtt tctg 2064

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<210> 22

<211> 570

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (28)... (489)

<400> 22

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agccggacgg ggatctgagc tggcagg atg aat gtg ggg gtg gca cac agc 51

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Met Asn Val Gly Val Ala His Ser

36/41

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gaa gta aac ccc aac acc cga gtg atg aat agc cga ggc atc tgg ctg			99
Glu Val Asn Pro Asn Thr Arg Val Met Asn Ser Arg Gly Ile Trp Leu			
10	15	20	
gcc tac atc atc ttg gta gga ttg ctg cat atg gtt cta ctc agc atc			147
Ala Tyr Ile Ile Leu Val Gly Leu Leu His Met Val Leu Leu Ser Ile			
25	30	35	40
ccc ttc ttc agc att cct gtt gtc tgg acc ctg acc aac gtc atc cat			195
Pro Phe Phe Ser Ile Pro Val Val Trp Thr Leu Thr Asn Val Ile His			
45	50	55	
aac ctg gct acg tat gtc ttc ctt cat acg gtg aaa ggg aca ccc ttt			243
Asn Leu Ala Thr Tyr Val Phe Leu His Thr Val Lys Gly Thr Pro Phe			
60	65	70	
gag act cct gac caa gga aag gct cgg cta ctg aca cac tgg gag caa			291
Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His Trp Glu Gln			
75	80	85	
atg gac tat ggg ctc cag ttt acc tct tcc cgc aag ttc ctc agc atc			339
Met Asp Tyr Gly Leu Gln Phe Thr Ser Ser Arg Lys Phe Leu Ser Ile			
90	95	100	
tct cct att gtg ctc tat ctc ctg gcc agc ttc tat acc aag tat gat			387
Ser Pro Ile Val Leu Tyr Leu Leu Ala Ser Phe Tyr Thr Lys Tyr Asp			
105	110	115	120
gct gcg cac ttc ctc atc aac aca gcc tca ttg cta agt gta ctg ctg			435
Ala Ala His Phe Leu Ile Asn Thr Ala Ser Leu Leu Ser Val Leu Leu			
125	130	135	

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ccg aag ttg ccc cag ttc cat ggg gtt cgt gtc ttt ggc atc aac aaa 483

Pro Lys Leu Pro Gln Phe His Gly Val Arg Val Phe Gly Ile Asn Lys

140

145

150

tac tgag ggatgggttt tgggacagct ccatgggcat ggggaaggca ctgaaacaga 540

Tyr

ggactataaaa acatccttct cttattctcc 570

<210> 23

<211> 1161

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (278)... (880)

<400> 23

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ggtgtggtgc cggtgggaac tgaggaagcg cccaaggaaa tgaaacacga tttccaaat 120

gaacttaatc tttcatgaga aactgaggat agagatgtca ataagcagcc actgtttcca 180

cctccccacc tgaagagcta ggaggacaac taaaagagc ctgactgcct tctcggaatg 240

aggagagagg aaaacagcaa cagtatcagt tttcaag atg gca gca tct atg 292

Met Ala Ala Ser Met

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cat ggt cag ccc agt cct tct cta gaa gat gca aaa ctc aga aga cca	340
His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu Arg Arg Pro	
10 15 20	
atg gtc ata gaa atc ata gaa aaa aat ttt gac tat ctt aga aaa gaa	388
Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp Tyr Leu Arg Lys Glu	
25 30 35	
atg aca caa aat ata tat caa atg gcg aca ttt gga aca aca gct ggt	436
Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr Thr Ala Gly	
40 45 50	
ttc tct gga ata ttc tca aac ttc ctg ttc aga cgc tgc ttc aag gtt	484
Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys Phe Lys Val	
55 60 65	
aaa cat gat gct ttg aag aca tat gca tca ttg gct aca ctt cca ttt	532
Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr Leu Pro Phe	
70 75 80 85	
ttg tct act gtt gtt act gac aag ctt ttt gta att gat gct ttg tat	580
Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp Ala Leu Tyr	
90 95 100	
tca gat aat ata agc aag gaa aac tgt gtt ttc aga agc tca ctg att	628
Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser Ser Leu Ile	
105 110 115	
ggc ata gtt tgt ggt gtt ttc tat ccc agt tct ttg gct ttt act aaa	676
Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Leu Ala Phe Thr Lys	
120 125 130	
aat gga cgc ctg gca acc aag tat cat acc gtt cca ctg cca cca aaa	724

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Asn Gly Arg Leu Ala Thr Lys Tyr His Thr Val Pro Leu Pro Pro Lys
 135 140 145
 gga agg gtt tta atc cat tgg atg acg ctt tgt caa aca caa atg aaa 772
 Gly Arg Val Leu Ile His Trp Met Thr Leu Cys Gln Thr Gln Met Lys
 150 155 160 165
 tta atg gcg att cct cta gtc ttt cag att atg ttt gga ata tta aat 820
 Leu Met Ala Ile Pro Leu Val Phe Gln Ile Met Phe Gly Ile Leu Asn
 170 175 180
 ggt cta tac cat tat gca gta ttt gaa gag aca ctt gag aaa act ata 868
 Gly Leu Tyr His Tyr Ala Val Phe Glu Glu Thr Leu Glu Lys Thr Ile
 185 190 195
 cat gaa gag taaccaaaaa aatgaatggt tgctaactta gcaaaatgaa gtt 920
 His Glu Glu
 200
 tctataaaga ggactcaggc attgctgaaa gagttaaag taactgtgaa caaataattt 980
 gttctgtgcc ttttgctgg tatatagcaa atactcaaaa agtattcaat aattcaatca 1040
 ataaatataa gtttcatctt acacgtaaga tacaggctctt atctctgat ggtgtgtcca 1100
 ttttgctgg tatataacag ataataaata tccagtgtca ataaatgtaa caataaaagt 1160
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<210> 24

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (58)... (627)

<400> 24

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Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala	
1 5 10 15	
atc cca ggg ggc ctc ggg gac agg gcg cca ctc aca gcc aca gcc cca	153
Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro	
20 25 30	
caa ctg gat gat gag gag atg tac tca gcc cac atg ccc gct cac ctg	201
Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu	
35 40 45	
cgc tgt gat gcc tgc aga gct gtg gct tac cag atg tgg caa aat ctg	249
Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu	
50 55 60	
gca aag gca gag acc aaa ctt cat acc tca aac tct ggg ggg cgg cgg	297
Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg	
65 70 75 80	
gag ctg agc gag ttg gtc tac acg gat gtc ctg gac cgg agc tgc tcc	345
Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser	
85 90 95	
cgg aac tgg cag gac tac gga gtt cga gaa gtg gac caa gtg aaa cgt	393

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Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
 100 105 110
 ctc aca ggc cca gga ctt agc gag ggg cca gag cca agc atc agc gtg 441
 Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val
 115 120 125
 atg gtc aca ggg ggc ccc tgg cct acc agg ctc tcc agg aca tgt ttg 489
 Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu
 130 135 140
 cac tac ttg ggg gag ttt gga gaa gac cag atc tat gaa gcc cac caa 537
 His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln
 145 150 155 160
 caa ggc cga ggg gct ctg gag gca ttg cta tgt ggg gga ccc cag ggg 585
 Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly
 165 170 175
 gcc tgc tca gag aag gtg tca gcc aca aga gaa gag ctc tagtcc 630
 Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu
 180 185
 tggactctac cctcctctga aagaagctgg ggcttgctct gacggctctcc actcccgtct 690
 gcaggcagcc aggagggcag gaagcccttg ctctgtgctg ccacccctgcc tccctcctcc 750
 agcctcaggg cactcgggcc tgggtgggag tcaacgcctt cccctctgga ctcaaataaa 810
 acccagtgc ctc 823